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RS da Silva,A.C.R., Febro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R., da Silva,A.C.R., Febro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R., da Silva,A.C.R., Dan Juuys,M.A., Almeida Jr.,N.F., Alves,L.M.C., Canaral,A.M., Bertolini,M.C., Canargo,L.E.A., Camartote,G., Cannavan,F., Cardozo,J.C., Canargo,L.E.A., Carabha,L.P., Glarelli,R.M.B. Coutinho,L.L., Carabha,L.P., Glarelli,R.M.B., Coutinho,L.L., Curaino-Santos,J.R., Ferrol,M.I.T., Formighieri,E.F., Franco,M.C., Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite Jr.,R.P., Lemos,E.G.M., Lemos,M.Y.F., Locali,E.C., Machado,M.A., Madeira,A.M.B.N., Martins,E.C., Machado,M.A., Mancha,V.K., Oliveira,M.C., Oliveira,M.C., Oliveira,M.C., Oliveira,M.C., Oliveira,M.C., Oliveira,M.R., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F., Ratis,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A., Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J., Menck, C.F.M., Novo, M.T.M., Novo, M.T.M., Novo, M.T.M., Novo, M.T.M., Novo, M.T.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Takita, M.A., Tamura, R.E., Teikeira, E.C., Tezza, R.I.D., Trindade dos Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubai, J.C. and Kitajima, J.P. /protein_id="AAM40526.1" /db_xref="051:211122144" /translation="WRILPISAGPLQPHAAAAPARATQRVSFMQLRRRLSSVLAGLPD TVVPEDEDDOPTLAEVMDAASDDHGEPALPTAPPCLDDASNRRQIARGDDGDALGRQIA /organism="Xanthomonas campestris pv. campestris str. ATCC 33913" ÷.⊹g Submitted (28-NOV-2001) Departmento de Bioquimica, Universidade c Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900, note-"identified by sequence similarity; putative; ORF Comparison of the genomes of two Xanthomonas pathogens with differing host specificities
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'note="identified by sequence similarity; putative; ORF

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AAQDAARRARERLAEI VAHACEQVLHGHDFAALYARAAQALDGALDEANALQVSVHPD
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Search completed: July 7, 2004, 23:54:59 Job time: 1897.13 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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July 7, 2004, 17:42:57 ; Search time 205.168 Seconds (without alignments) 14535.578 Million cell updates/sec

US-10-018-786-7 702 Title: Perfect score:

1 atgogtotttggotgaggto......cggtgooggatgcttgctga 702 Sequence:

Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0

3373863 seqs, 2124099041 residues

Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:* geneseqn2003as:* genesegn2003bs:*genesegn2003cs:* geneseqn2001as:*geneseqn2001bs:* genesedn2002s:* 8: 9: 10: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

SUMMARIES

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Ω	ABL57895	VAD5 4645	AAD5 4236	AAD54230	VAX53491	AAL61177	AAL61224
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Aad55817 Micromono Aad55810 Micromono	3491 Huma	2	.187 A	31 B	2129 Benzoc	88	5519 Human	თ	.38 Lei	7558 Le	225621 Lei	85 Lei	5022 Lei	Abk81733 Leishmani	4	Adb78770 Leishmani	51171 Ac	6049 Pr	5819	2810	85	7186	ø	3 Act	4 Act	97	71 S.	1197 A	636	3873	4	968	9963	d24026 Human p	6363 DNA enc	Abz11989 Human pol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to new Xanthomonas campestris bacteria strains made non-virulent by inactivation of at least one virulence gene but which have retained the capacity to produce exc-polysaccharides (preferably xanthan gum, one such virulence gene deleted to produce the bacterial strains was the hrpB3 gene (Hypersensitive Reaction and Pathogenicity). The hrp genes are sesential for pathogenicity, in plants. The present sequence is a partial sequence of the hrpB3, used in an example from the invention. (Updated on 11-SEP-2003 to standardise OS
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                           Xanthomonas campestris; pv vesicatoria.
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                                                                                                                                                                                                                                             22-JUN-1999; 99FR-00007963
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Search completed: July 7, 2004, 21:07:53 Job time: 209.168 secs

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Run on:	<pre>July 7, 2004, 20:18:17 ; Search time 1351.57 Seconds (without alignments) 15510.569 #111on cell upd</pre>
Title: Perfect score: Sequence:	US-10-018-786-7 702 1 atgogrotttggctgaggtcggtgccggatgcttgctga
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	27513289 segs, 14931090276 residues
Total number of	hits satisfying chosen parameters: 55026578
Minimum DB seq Maximum DB seq	seq length: 0 seq length: 2000000000
Post-processing:	: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	EST:: 1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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